

Kb
 9.5 →
 7.5 →
 4.4 →
 2.4 →
 1.4 →
 0.24 →

Non-fruited plants
 L
 S
 R

Fruited plants
 L
 S
 R

G
 G/R
 R/G
 R
 B

← 0.89

Figure 1

The image displays a gel electrophoresis result for restriction enzyme digestion. On the left, molecular weight markers are indicated in kbp: 23.13, 9.41, 6.55, and 4.36. The gel is organized into three main sections for different enzymes: *EcoRI*, *BamHI*, and *HindIII*. Each enzyme section contains five lanes, numbered 1 to 5 at the top. Lane 1 in each section appears to be a DNA ladder, showing multiple bands corresponding to the markers. Lanes 2 through 5 show the results of digestion with the respective enzyme. For *EcoRI*, lane 2 shows a prominent band at approximately 9.41 kbp. For *BamHI*, lane 2 shows a prominent band at approximately 23.13 kbp. For *HindIII*, lane 2 shows a prominent band at approximately 9.41 kbp. The background of the gel is dark, and the bands are bright white.

2/11

1 CAGCATTCCA AGAGGAAAAA AAACATGATC AAGAAGTAAT TACTACAAAA
51 GAGGAAGCTG TAGTAGTAAC TGCACCACCA CCATCAGAAA CAGCAGAGCC
101 AGCTGCAGCT GTTGTTGCCG AGGAAGAGAC AACAAAGGAG CAAGAAGAGC
151 CGCCAGCAGT ATCGGCCGAG GAACCTGTGG CCCCAGCTGA AGTAGAGACA
201 AAGGTGGAAG TTACAGAAGA ACCACCAAAA GTTGAGGAGA AACCAGCAGA
251 AGTAGAGGAG GCTCCAAAGG AAACAGTAGA AACAGAACCA GCTGTTGAGA
301 AGACCATCAA GGAGGAAACT GTAGAGGACT CTGTCGTGGC ACCTGCTCCC
351 GAACCGGAAG CCGAAGTCCC AAAAGAGAAG GTAATTGCTA CTACTGAAAC
401 TACTGAGGAA GAAGAAAAAG TGGCAGTTGA AGAAGTTGAA GTGAAAGTTG
451 AAACAGAGGA GGGAGAAGTT ACTGAGGAGA AGACTGAGTA AAATAAGTTG
501 TACAACTATT TTATGCACGC CTTATTTTCT CAATTGGAAG TTTATAATGT
551 AGTGGGCTTT TGGTAATATT TGGGGGTTTA ATAAGTGGTT TAAGTGGGTT
601 AAGGCTTTTT TGGAATTTAG ATATTTGGGT AAAGGCCTAC TTGAACAAAA
651 CATAGAAATT TGGCACACAT GGGTAAAAGT CAACTTTGT TGAGGATGTT
701 TTCTTGTTGG TTAAATGTGT GTGCCAAGTA GTAGAATGTG GTGGTTGTAA
751 TGTAAGTTCT CAAGTAGGGT TTATGAGTCC TAGTATTATG CTTGATTGTA
801 TGTTGATATG AAAATGGGGG TATGTTGGCT TTGAATAAAA GTTTTAAATT
851 TTATAAAAAA AAAAAAAAAA AAAAAAAAAA AA

Figure 3

1 AAACAACAACTTTTTTCATCAATCTTCTTTCTTTAATCATCACCATGTCGAGCTGCGGAA 60
 T T N F F I N L L S L I I T M S S C G N
 61 ACTGCGACTGTGCCGACAAGACCAACTGCCCAAAGAAGGGAAACAGCTACGGCTTTGACA 120
 C D C A D K T N C P K K G N S Y G F D I
 121 TCATTGAGACCCAGAAGAGCTACGATGACGTCGTGGTGATGGATGTTTCAGGCAGCTGAGA 180
 I E T Q K S Y D D V V V M D V Q A A E N
 181 ATGATGGCAAGTGCAAGTGCGGCCCCGAGCTGCAGTTGTGTGGGCTGCAGCTGTGGTCATT 240
 D G K C K C G P S C S C V G C S C G H *
 241 AAGTTAAACACAACATTATCATGTTATAGTGAATAATGATGTGTGTGATGAATATAGGTG 300
 301 AAAAATCTGTGGTGTGATAAAAACCGTTGGTGAATAAATAGGTGTATATTTTCGTGTGCAC 360
 361 CTTCTACGAGTACTTGTGCTTGTGGGTGAAAGAAATATGCACCTAAGTGTGAGTTGTTT 420
 421 TCCGTGTTTTTTCGCCGTGTCCCTTGTAATGGTCATGTTTGTGTTTTCTTGTGTTAAATT 480
 481 AAATGAAGTAGTAATGTTATGTAAAAA 519

Figure 5

1 GGAGGAGATCACCAGTTCCACCAACACGTCGTCGTAATGAGACACGGCGATCGGATAGAC 60
R R S P V P P T R R R N E T R R S D R Q

61 AACTTCGAGCCACTGTGGGTGAAGACGGCGGCGAACGATGGGACCCACCCTTGGTCGATG 120
L R A T V G E D G G E R W D P P L V D E

121 AAGGCAAGCTCCGTACCTTCCGGACAGGTCTGAAGCTCCGAACCAATTTTGATTTTCCGA 180
G K L R T F R T G L K L R T N F D F P I

181 TCCATCGTGTCTTTGTATCACCTTTCCTCCGGTGCGTACAGACAGCATCGGAAGTCATCT 240
H R V F V S P F L R C V Q T A S E V I S

241 CCGCTCTCTGCGCCGTCGACGATATTCCCGCCACCCTAATAGAGGCGATCAAGTACAAA 300
A L C A V D D I P A T T N R G D Q V Q I

301 TCGATCCATCCAAGATCAAGGTCTCTATTGAGTATGGATTATGTGAAATGTTGAACATGC 360
D P S K I K V S I E Y G L C E M L N M Q

361 AAGCCATAAGACTTGGTATGGATTTTCAGCAATGGGAATTGGGGTTTCGATAAATCACACC 420
A I R L G M D F S N G N W G F D K S H L

421 TTGAATCAACATTCCCAAGTTGGGACGGTGGATCATAGTGTGGAACCACTCTATAAAGAGA 480
E S T F P V G T V D H S V E P L Y K E M

481 TGCCAAAATGGGAAGAGACAGTCAATGGCGCAAGGGCCAGATATGAAGAGGTTATTCAGG 540
P K W E E T V N G A R A R Y E E V I Q A

541 CCCTAGCAGATAAAATACCCACGGAGAACTTGTTGCTTGTTACACATGGGGAAGGAGTTG 600
L A D K Y P T E N L L L V T H G E G V G

601 GCGTTGCAGTTTCTGCCTTCATGAAGGATGTTACAGTGTACGAAGCCGATTATTGTGCCT 660
V A V S A F M K D V T V Y E A D Y C A Y

661 ATACACACGCAAGAAGATCCATTGTCTTGGGCAAAAACCAGTCATTTACTGCTGAAAAC 720
T H A R R S I V L G K N Q S F T A E N F

721 TTGAAGTATTACCAAAAACAAGGCCAAACTGGTGTGTCAGTTACGTCCTTGAACAGCATTGAT 780
E V L P K Q G Q T G V S Y V L E Q H *

781 GGAAGTGTATGACCTAATTGTGGCAGCCGATGATTACAGAAACAATTTCCACACCTTTTT 840
841 TCTTTTTTTCGGGCATTTGCCTACATTTTATAATTAATTAGGCATTCTCATAGCTAAGGCT 900
901 CATTGGATTACATCCCTACTTGTTTAAAGGAGACTTTGATTTGTTGCCTCCAAACAGAA 960
961 CATATGTTGCTGTGTCCATCAGCTTTTTTTTAACTGGGATTTCTATTTTTTACAGTGTGTAA 1020
1021 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1046

Figure 6

1 GTTGATGGCAGATGTGACCAACTCAGGAAAAATGCCAGGGTTGTTGCAATTGATTCTTAC 60
V D G R C D Q L R K N A R V V A I D S Y

61 GAAGATGTTTCCTTTGAACGATGAGAACGCATTGAAAAAGGCAGTGGCTAGTCAGCCTGTG 120
E D V P L N D E N A L K K A V A S Q P V

121 CGCGTCGCCATTGAAGGAGGTGGCAGGGATTTCCAACCTCTATCAATCAGGCGTCTTTACT 180
R V A I E G G G R D F Q L Y Q S G V F T

181 GGATCATGTGGGACGGCCCTAGACCATGGTGTGGCTGCTGTTGGGTATGGCACAGAAAAT 240
G S C G T A L D H G V A A V G Y G T E N

241 GGTGTGGATTACTGGATTGTAAGGAACTCATGGGGTGCAAGCTGGGGAGAGAGCGGCTAC 300
G V D Y W I V R N S W G A S W G E S G Y

301 ATCAGGATGGAACGTAATCTGGCAGGCACAGCTACGGGCAAATGTGGTATTGCAATGGAA 360
I R M E R N L A G T A T G K C G I A M E

361 GCCTCTTACCCTATTAAGAAAGGCCAAAATCCCCCAAACCCAGGACCATCTCCTCCATCT 420
A S Y P I K K G Q N P P N P G P S P P S

421 CCAATAAAGACCTCCAACAGTTTTTGTGACAATTACTATACCTTGGCTGAAAGCACCCTT 480
P I K T S N S F V T I T I P W L K A P L

481 GCTGCTGTCTATTTGAGTTTGGCAGGTATTGCTTCGAGTGGGGATGTTGCCCACTCGAGG 540
A A V Y L S L A G I A S S G D V A H S R

541 CTGCCACTTGCTGTGATGACCATTACAGTTGCTGCCCACATGAGTATCCCATCTGCAACC 600
L P L A V M T I T V A A H M S I P S A T

601 TTAATGCAGGGACGTGTATGATGAGAAGGACAACCCATTGAGTGTGAAGGCATTGAAGCG 660
L M Q G R V *

661 TACTCCCGCTAAACCTCATTGGGCCTTTGGGAACCGTGGCAAGAGCAGCAGTGCTTAAGA 720
721 ACATTGTGTCATCTATACAGTGAAAGTAAAACGAGGATGAAAAGTTGTATCAGGCAGGGC 780
781 TTGATGATCTCCTCGGTTTTATAGTACCGCATACCCCTCATTCTCCATTAAGGTCATATAC 840
841 ATATGGACGGTTTATCAAAGTTTATTTCAGATGCTAATTATGTATATATCATTCTCAGTC 900
901 TCTGTATTTTCATTTTAAACGAGAACATAAACAGATCGTTATCAGCTACCAATTTCCACTGT 960
961 AAATCACGTTATCAATTATTTACTGGCCTCGCTGAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1017

Figure 7

1 CGGTTCAATCGCTGGATCAATCGAGCATATGGCGATGTATCCGGTTGATACGCTTAAAC 60
 G S I A G S I E H M A M Y P V D T L K T
 61 TCGCATAACAGGCTATTGGGTCATGTTCCGGCTCAATCCGCCGGTCTCCGACAAGCCCTTGG 120
 R I Q A I G S C S A Q S A G L R Q A L G
 121 GTCGATACTGAAAGTTGAAGGTCCCGCCGGACTTTACCGTGGCATTGGTGCAATGGGTCT 180
 S I L K V E G P A G L Y R G I G A M G L
 181 CGGTGCAGGACCAGCTCACGCAGTGTATTTCTCCGTTTACGAGATGTGTAAGGAGACTTT 240
 G A G P A H A V Y F S V Y E M C K E T F
 241 TTCTCATGGTGATCCGAGCAATTCCGGTGCGCAGCCCGTTTCGGGGGTGTTCCGCGACGGT 300
 S H G D P S N S G A H A V S G V F A T V
 301 GGCAAGCGACGCGGTGATTACGCCGATGGATGTGGTGAAACAGAGGTTGCAGTTGCAGAG 360
 A S D A V I T P M D V V K Q R L Q L Q S
 361 CAGTCCGTACAAGGGTGTGTTGATTGCGTGAGGAGGGTGTGTTGGTAGAAGAAGGGATTGG 420
 S P Y K G V V D C V R R V L V E E G I G
 421 CGCATTTTACGCATCTTATCGAACAACGTGGTTCATGAATGCCCCGTTTACGGCCGTTCA 480
 A F Y A S Y R T T V V M N A P F T A V H
 481 CTTCCGCCACATATGAAGCCACGAAGAAAGGGTGTGTTGGAGGTGTCGCCGGAGACTGCGAA 540
 F A T Y E A T K K G L L E V S P E T A N
 541 CGATGAGAATTTGTTAGTGCATGCTACTGCTGGTGCTGCTGCTGGAGCTTTGGCTGCAGT 600
 D E N L L V H A T A G A A A G A L A A V
 601 AGTAACCACTCCACTAGATGTTGTCAAACTCAGTTGCAGTGCCAAGGTGTTTGCGGATG 660
 V T T P L D V V K T Q L Q C Q G V C G C
 661 CGACAGATTTTCTAGCAGTTCGATTTCAGGATGTTATAGGAAGCATAGTGAAGAAAAATGG 720
 D R F S S S S I Q D V I G S I V K K N G
 721 ATATGTCGGGTTAATGAGGGGGTGGATTCCCAGAATGCTATTTTCATGCTCCTGCTGCAGC 780
 Y V G L M R G W I P R M L F H A P A A A
 781 AATCTGCTGGTCTACTTATGAAGCCTCCAAAACATTCTTTCAAAAACCTCAATGAGAGCAA 840
 I C W S T Y E A S K T F F Q K L N E S N
 841 TAGCAACAGCTCAGTTACCTAAGATTTTCATATGTTTTTGTGCTCTACTAGGCTTATCCA 900
 S N S S V T *
 901 AAATCATGTCGATTGGTTTCACTTCACCACAGTTGCCATGAACAACCTCAAAGCATCGAAT 960
 961 TTTACATGTATATTATGCAATCTAGATGCTTCTTGATATTTATTTTTTCTTTTC 1020
 1021 CAACTTTTGTAATTAGAATTAGCTACTATGGTTATGGCATGGAGTGTTTTATAATTGCTA 1080
 1081 ATATCATCGTATAAGCAATGCTATTTGAGAAATTGTGGTGTAAGGTTAGAGTAATGTTAT 1140
 1141 TTGCACAATCCACTTACATAGACCGCGGGACTCATTTAAAAA 1195

Figure 8

Sequence

1 GATGTTTATAT TGGGATGGA AAGTTTCADA TTACTCTGATA TGTAACTCTC AACAAATCA AGCTTTTGTAT CATATAAATC GAACCAACA CACAATAATT
 101 ATGAATTTCT TTGACICTTT GTCCTGTAC CNAATACGC ACACACAAA AAATTCCTTT TGIATTAAT TCGTTTTTTA TTTTTTTAAC GTTTTGGTAT
 201 TCAACATCA TATAGTAAG GGGGAATATT NTTCGGACTC CTCCAAAAC TTATGACATT GTGATTACAC ATTGGAATGA CAGAAGTTTT TGATGAAGTG
 301 CCAATATCAA TCTTTTCTTA ATTGCTTCAT AAAGGGTGT TTTGTAATTA AAAGAAGAT AAGGAATTT AGCAAGAAGT GCATTATTGG GACTGGTATA
 401 TATGACAAGG ATCTGACGTG GCAAGAAGG AAGTGGTTC CTGATCAGG TGTGTCCAT CTGTCAATAT TCTTCAAAAG AGAGTCCACC ATCTCATAGA
 501 TGAGATTAG AAGTGGTGT CCACAAAAA ATATGACACA ACCCATCCAT GAACCAATAA AATCATGACA GGTATCATAT TCTTTCTCTC
 601 AAGATATAA TACCTATTAG TGCTTTTAA ACCTGGCTAA CTTTGCAATT CTGTCAATTT GGTGACTTTT TATTGCCCAA TTGTGGCTTG AAGGAAATAA
 701 AAAGGAAGT CTTTTTCTTG AACCCATAG GAGCAATTT CAATGAGGA GATGAGGAGG ATGCGGTGG AGAATTGATA CGGATCTTCT
 801 TTAATTGGTA TATGTAAATC ACTCAGAAC ACGTATACCA TATATGCATC AATGTCAATG TCACAGAAA CGTAACTCAC GAACACATTT CGTAACATGC
 901 ATGCACCAAT CATACATTAT AACATAGTGT TACGACAATA AAAGAICTTT AGTCGTAAGA GCATTAGTCT GTGACAAGAA CAAAAACGTG GATTCCTCAAC
 1001 CTAAGAAGG GTATATCTTT TATTCATATA TCTACTTTTG ATATGACCTA AACCTTGTGT CACCCACAA ATCGATANTT GTTTGACTTG
 1101 TGTTGGATGA GAATATGAT GAGACTGACC ATTAGTTTTA GCCGGATGTG ATTTGGGTAT ATTGATGACA ATATAAGATA TATAAAACTT GAACAAACA
 1201 ATTCTCAAC AATTAATCT AAGATANT CTCTCTTCA; NTGATTAAT AAATGATGA ATATCCGTG AGTACCCCA ATAAATTAAA ATCTCCAGCA
 1301 AATACGTGA TTCTTTTCT TCGAAGCGAA ATCTCTTCT TCCAAACACC TTAACAATG TAAATTCCT TAGTAAGATT AAATTTGAAA TGATAACACA
 1401 AGAGTGAATA AAGGTCAAG TCACCTACTT ACCCAACTGC ACAAACACA CAAGCACACA TCCAAAAGTA GTAGTATGAT TACACACATT TGAANAANTG
 1501 ACCTCCATTA TTTTAGCCAC CTCTCTTCTA AAAAGNITA CAACAATTT ACTCTATCA TTATTATAA AATAGTAGCA TAACCTCATC TCCAATCCAC
 1601 ACCATATATT TTACATTATT GCCAAACATG CTAAAGCTT CTGTATTCA GTGAATATGT GGTGTCAANT CCCAGATTC TTCATGTGCC CTCTCTCTCT
 1701 CTCTCTCTCT CTCTCTCTCT CCTCCTCTC ATCAACTTGA GGGCTTTAGG ACCTCTATAT AAACCTCTCT CAATTGATCA TCTCTGC

← Putative promoter sequence

Figure 9

2641 AGGAAACTGTAGAGGACTCTGTCGTGGCACCTGCTCCCGAACC GGAAGCCGAAGTCCCAA 2700
 E T V E D S V V A P A P E P E A E V P K
 2701 AAGAGAAGGTAATTGCTACTACTGAACTACTGAGGAAGAAGAAAAAGTGGCAGTTGAAG 2760
 E K V I A T T E T T E E E E K V A V E E
 2761 AAGTTGAAGTGAAAGTTGAAACAGAGGAGGGAGAAGTTACTGAGGAGAAGACTGAGTAAA 2820
 V E V K V E T E E G E V T E E K T E *
 2821 ATAAGTTGTACAAC TATTTTATGCACGCCTTATTTTCTCAATTGGAAGTTTATAATGTAG 2880
 2881 TGGGCTTTTGGTAATATTTGGGGGTTTAATAAGTGGTTTAAGTGGGTTAAGGCTTTTTTG 2940
 2941 GAATTTAGATATTTGGGTAAAGGCCTACTTGAACAAAACATAGAAATTTGGCACACATGG 3000
 3001 GTAAAAGTCAAAC TTTGTTGAGGATGTTTTCTTGTTGGTTAAATGTGTGTGCCAAGTAGT 3060
 3061 AGAATGTGGTGGTTGTAATGTAAGTTCTCAAGTAGGGTTTATGAGTCCTAGTATTATGCT 3120
 3121 TGATTGTATGTTGATATGAAAATGGGGGTATGTTGGCTTTGAATAAAAGTTTTTAATTTT 3180
 3181 ATATAATAAGTGTATTTTGTTTAATATCATTCTTTCATTCTCTCGGATCAACTACTGAT 3240
 3241 CATCGCCTTGGTAAAGCTATTGCCTCACCAACTAGCTAATCGAACGCGAGCCC 3292

Figure 10b